Supplementary Table S6. Differential gene expression according to tumor location

	logFC	P-Value	FDR
ATM	-0.588	<0.001	0.005
PMS1	-0.809	<0.001	0.017
MPG	-0.480	0.001	0.026
POLL	-1.470	0.001	0.026
DNAJB2	-0.442	0.001	0.026
RPA1	0.427	0.002	0.041
DNAJC5	-0.503	0.004	0.072
XRCC5	-0.874	0.005	0.072
TOP3B	-1.297	0.006	0.072
PARP1	0.360	0.006	0.075
RAD21	0.379	0.008	0.078
POLD3	0.405	0.008	0.078
PARP3	-0.995	0.009	0.079
NEIL3	0.513	0.010	0.079
DNAJC4	-0.309	0.010	0.079
DNAJB8	-0.897	0.011	0.079
PMS2	-0.391	0.012	0.083
DNAJC7	-0.475	0.013	0.084
RAD51D	0.297	0.016	0.089
BRIP1	0.536	0.016	0.089
TDG	0.266	0.016	0.089
DNAJC15	-0.466	0.017	0.092
MLH3	-0.266	0.018	0.092
RAD52	-0.562	0.028	0.137
MRE11A	-0.272	0.039	0.185
MSH5	-0.633	0.046	0.205
DNAJC16	-0.507	0.048	0.205
ERCC1	-0.216	0.049	0.205

FC: fold change; FDR: false discovery rate. A negative fold change means that the gene is overexpressed in somatic cases